

**Angell, Jon E**

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**From:** Angell, Jon E  
**Sent:** Friday, September 01, 2006 2:37 PM  
**To:** STIC-Biotech/ChemLib  
**Subject:** Sequence Search Request 10/674,836

## Sequence Search Request 10/674,836

Examiner# : 78697  
Art Unit : 1635  
Phone Number: 571-272-0756  
Mailbox & Bldg/Room Location: REMSEN 2C18  
Results Format Preferred (circle): DISK

I would like to have a standard search performed using the following :

- 1) nucleotides 13306 through 13509 of SEQ ID NO:1
- 2) nucleotides 13428 through 13509 of SEQ ID NO:1

In addition to the standard search of #1 and #2 above, please include searches for #2 (13428-13509 of SEQ ID NO:1) that only return hits that are A) 400-900 nucleotides in length, B) 200-400 nucleotides in length, and c) 100-200 nucleotides in length.

Please contact me by phone or email if you have any questions.

Thanks,  
Eric

**J. Eric Angell**  
Art Unit 1635  
Office: REMSEN 2D20  
mailbox: REM 2C18  
571-272-0756

[Go Back to previous page](#)

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OM nucleic - nucleic search, using sw model

Run on: September 5, 2006, 17:23:08 ; Search time 5278.32 Seconds  
 (without alignments)  
 2161.207 Million cell updates/sec

Title: US-10-674-836-1\_COPY\_13306\_13509  
 Perfect score: 204  
 Sequence: 1 gtggcggagggactggggac.....gcagcgctgcgtcctgctgc 204

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : EST:\*  
 1: gb\_est1:\*  
 2: gb\_est3:\*  
 3: gb\_est4:\*  
 4: gb\_est5:\*  
 5: gb\_est6:\*  
 6: gb\_htc:\*  
 7: gb\_est2:\*  
 8: gb\_est7:\*  
 9: gb\_est8:\*  
 10: gb\_est9:\*  
 11: gb\_gss1:\*  
 12: gb\_gss2:\*  
 13: gb\_gss3:\*  
 14: gb\_gss4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	No.	Score	% Match	Query Length	DB ID	Description
c	1	70.6	34.6	666	13	CW946150 TcB28.4_B
c	2	70.6	34.6	855	1	AL573255 AL573255
c	3	69.2	33.9	890	13	CL493826 SAIL_586_
	4	69	33.8	1081	13	CL464716 SAIL_1225
	5	69	33.8	1328	14	AG320910 Mus muscu
	6	68.6	33.6	934	13	CL477947 SAIL_283_

	7	68.4	33.5	572	11	BZ050840	BZ050840 jnr64d12.
c	8	68.4	33.5	1806	12	CG756794	CG756794 P051-4-G0
	9	68.2	33.4	675	11	BZ050815	BZ050815 jnr64a12.
	10	67.2	32.9	458	14	CNS00D2T	AL060559 Drosophil
c	11	67.2	32.9	916	3	BU197009	BU197009 AGENCOURT
	12	67.2	32.9	1051	4	CB206210	CB206210 AGENCOURT
c	13	67	32.8	566	14	CNS03JN0	AL247077 Tetraodon
	14	67	32.8	898	5	CK414740	CK414740 AUF_IpGil
c	15	67	32.8	1330	12	CL063297	CL063297 CH216-99P
c	16	67	32.8	1675	14	AG360980	AG360980 Mus muscu
	17	66.6	32.6	579	14	CNS04OTC	AL300441 Tetraodon
	18	66.6	32.6	921	13	CL489959	CL489959 SAIL_531_
	19	66.6	32.6	949	13	CL465953	CL465953 SAIL_1249
	20	66.6	32.6	969	13	CL477043	CL477043 SAIL_267_
c	21	66.6	32.6	988	3	BU183975	BU183975 AGENCOURT
	22	66.6	32.6	1374	14	AG435756	AG435756 Mus muscu
	23	66.6	32.6	1695	12	CC290874	CC290874 CH261-172
c	24	66.4	32.5	822	14	AG430981	AG430981 Mus muscu
	25	66.4	32.5	1040	13	CL466687	CL466687 SAIL_125_
c	26	66.2	32.5	881	4	BX427015	BX427015 BX427015
c	27	66.2	32.5	897	13	CL470675	CL470675 SAIL_146_
c	28	66.2	32.5	933	14	CNS006XG	AL066047 Drosophil
	29	66.2	32.5	1026	3	BU900073	BU900073 AGENCOURT
	30	66.2	32.5	1128	3	BU841360	BU841360 AGENCOURT
	31	66	32.4	774	14	AG479706	AG479706 Mus muscu
c	32	66	32.4	1066	4	CB905393	CB905393 tric074xd
c	33	66	32.4	1066	5	CF876920	CF876920 tric074xd
c	34	65.8	32.3	675	14	CR152762	CR152762 Reverse s
c	35	65.8	32.3	902	2	BI956545	BI956545 HVSMEn000
	36	65.8	32.3	1008	3	BQ942600	BQ942600 AGENCOURT
	37	65.8	32.3	1109	13	CL515456	CL515456 SAIL_8_E1
c	38	65.8	32.3	1289	12	CL147104	CL147104 ISB1-156E
c	39	65.8	32.3	1622	13	CL476695	CL476695 SAIL_258_
c	40	65.8	32.3	1691	14	AG341104	AG341104 Mus muscu
c	41	65.6	32.2	881	9	DN565434	DN565434 91010253
c	42	65.6	32.2	957	3	BQ423706	BQ423706 AGENCOURT
	43	65.6	32.2	988	13	CL477397	CL477397 SAIL_272_
c	44	65.4	32.1	792	14	AG449674	AG449674 Mus muscu
c	45	65.4	32.1	856	2	BI952342	BI952342 HVSMEm000

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OM nucleic - nucleic search, using sw model

Run on: September 5, 2006, 17:48:56 ; Search time 127 Seconds  
(without alignments)  
1064.709 Million cell updates/sec

Title: US-10-674-836-1\_COPY\_13428\_13509  
Perfect score: 82  
Sequence: 1 ccctcccagcccctcccctt.....gcagcgctgcgtcctgctgc 82

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2281053 seqs, 824500224 residues

Total number of hits satisfying chosen parameters: 206322

Minimum DB seq length: 200

Maximum DB seq length: 400

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA\_New:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*  
8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq1:\*  
9: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq2:\*  
10: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match					
	1	77.8	94.9	314	7	US-11-416-160-8	Sequence 8, Appli
	2	30.6	37.3	201	6	US-10-284-444-25832	Sequence 25832, A
c	3	25.6	31.2	379	8	US-11-266-748A-177592	Sequence 177592,
	4	25.6	31.2	379	8	US-11-266-748A-248086	Sequence 248086,
	5	25.6	31.2	393	8	US-11-266-748A-256733	Sequence 256733,
c	6	25.6	31.2	393	8	US-11-266-748A-317250	Sequence 317250,
	7	25.4	31.0	219	8	US-11-301-554-1124	Sequence 1124, Ap
c	8	25.4	31.0	294	8	US-11-301-554-1199	Sequence 1199, Ap
c	9	24.4	29.8	383	8	US-11-266-748A-37162	Sequence 37162, A
c	10	24.4	29.8	398	8	US-11-266-748A-85337	Sequence 85337, A
	11	24.4	29.8	398	8	US-11-266-748A-138148	Sequence 138148,
c	12	24.2	29.5	315	8	US-11-266-748A-249652	Sequence 249652,

	13	23.8	29.0	262	8	US-11-266-748A-75445	Sequence 75445, A
	14	23.8	29.0	262	8	US-11-266-748A-108903	Sequence 108903,
c	15	23.8	29.0	262	8	US-11-266-748A-128256	Sequence 128256,
c	16	23.8	29.0	287	8	US-11-266-748A-410144	Sequence 410144,
c	17	23.6	28.8	201	6	US-10-284-444-35034	Sequence 35034, A
	18	23.6	28.8	285	8	US-11-266-748A-100971	Sequence 100971,
c	19	23.6	28.8	285	8	US-11-266-748A-153782	Sequence 153782,
	20	23.6	28.8	303	8	US-11-266-748A-358392	Sequence 358392,
c	21	23.6	28.8	303	8	US-11-266-748A-441771	Sequence 441771,
	22	23.6	28.8	313	8	US-11-266-748A-4261	Sequence 4261, Ap
	23	23.6	28.8	365	8	US-11-266-748A-94534	Sequence 94534, A
c	24	23.6	28.8	365	8	US-11-266-748A-147345	Sequence 147345,
	25	23.6	28.8	380	8	US-11-266-748A-33852	Sequence 33852, A
c	26	23.4	28.5	239	8	US-11-266-748A-410551	Sequence 410551,
	27	23.4	28.5	294	8	US-11-266-748A-410156	Sequence 410156,
c	28	23.4	28.5	390	6	US-10-374-780A-1629	Sequence 1629, Ap
c	29	23.2	28.3	201	6	US-10-284-444-31621	Sequence 31621, A
c	30	23.2	28.3	384	8	US-11-266-748A-353381	Sequence 353381,
	31	23.2	28.3	384	8	US-11-266-748A-436760	Sequence 436760,
	32	23	28.0	353	8	US-11-266-748A-37533	Sequence 37533, A
	33	23	28.0	385	8	US-11-266-748A-250338	Sequence 250338,
	34	23	28.0	385	8	US-11-266-748A-274932	Sequence 274932,
c	35	23	28.0	385	8	US-11-266-748A-310855	Sequence 310855,
	36	22.8	27.8	201	6	US-10-284-444-34669	Sequence 34669, A
c	37	22.8	27.8	328	8	US-11-266-748A-296551	Sequence 296551,
c	38	22.6	27.6	338	8	US-11-266-748A-82659	Sequence 82659, A
c	39	22.6	27.6	338	8	US-11-266-748A-111385	Sequence 111385,
	40	22.6	27.6	338	8	US-11-266-748A-135470	Sequence 135470,
	41	22.6	27.6	389	6	US-10-953-349-31775	Sequence 31775, A
	42	22.4	27.3	201	6	US-10-284-444-35227	Sequence 35227, A
c	43	22.4	27.3	238	8	US-11-266-748A-355222	Sequence 355222,
c	44	22.4	27.3	238	8	US-11-266-748A-385212	Sequence 385212,
	45	22.4	27.3	238	8	US-11-266-748A-438601	Sequence 438601,

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OM nucleic - nucleic search, using sw model

Run on: September 5, 2006, 17:23:08 ; Search time 2121.68 Seconds  
(without alignments)  
2161.207 Million cell updates/sec

Title: US-10-674-836-1\_COPY\_13428\_13509  
Perfect score: 82  
Sequence: 1 ccctcccagcccctcccctt.....gcagcgctgcgtcctgctgc 82

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est3:\*  
3: gb\_est4:\*  
4: gb\_est5:\*  
5: gb\_est6:\*  
6: gb\_htc:\*  
7: gb\_est2:\*  
8: gb\_est7:\*  
9: gb\_est8:\*  
10: gb\_est9:\*  
11: gb\_gss1:\*  
12: gb\_gss2:\*  
13: gb\_gss3:\*  
14: gb\_gss4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
c	1	36.2	44.1	1352	7	BE880315	BE880315 601490686
	2	36	43.9	935	2	BG863518	BG863518 602798802
	3	34.6	42.2	1278	5	CK232592	CK232592 ILLUMIGEN
	4	34.2	41.7	1283	13	CL509378	CL509378 SAIL_811
	5	34	41.5	1008	14	AG149215	AG149215 Pan trogl
	6	33.8	41.2	1151	3	BM927078	BM927078 AGENCOURT
c	7	33.6	41.0	463	5	CJ132427	CJ132427 CJ132427
c	8	33.6	41.0	999	14	AG387695	AG387695 Mus muscu

	9	33.4	40.7	409	8	CN274427	CN274427 170005313
c	10	33.4	40.7	1253	9	DN430435	DN430435 LIB4217-0
c	11	33.2	40.5	717	13	CZ666881	CZ666881 OM_Ba022
c	12	33.2	40.5	1077	3	BQ649061	BQ649061 AGENCOURT
	13	33.2	40.5	1761	3	BM808747	BM808747 AGENCOURT
	14	33	40.2	485	5	CD893097	CD893097 G118.122N
	15	33	40.2	538	4	CA680753	CA680753 wlm24.pk0
	16	33	40.2	579	4	CA632959	CA632959 wle1n.pk0
	17	33	40.2	641	5	CD926836	CD926836 GR45.100C
c	18	33	40.2	837	14	CT231335	CT231335 Sus scrofa
c	19	33	40.2	1119	5	CK215573	CK215573 FGAS02753
c	20	32.8	40.0	704	8	CO959189	CO959189 AGENCOURT
	21	32.8	40.0	795	14	AG310060	AG310060 Mus muscu
c	22	32.8	40.0	859	14	AG282470	AG282470 Mus muscu
	23	32.8	40.0	967	14	CNS00IYE	AL075395 Drosophil
c	24	32.6	39.8	468	14	CNS03ZNE	AL267827 Tetraodon
	25	32.6	39.8	1116	13	CL471067	CL471067 SAIL_155_
c	26	32.4	39.5	634	13	CZ615527	CZ615527 OM_Ba014
c	27	32.4	39.5	828	2	BG781046	BG781046 SEAUMC001
c	28	32.4	39.5	839	13	CW673918	CW673918 OP_Ba006
c	29	32.4	39.5	851	2	BI958166	BI958166 HVSMEn001
c	30	32.4	39.5	900	7	BB901768	BB901768 BB901768
	31	32.4	39.5	1026	3	BU900073	BU900073 AGENCOURT
	32	32.4	39.5	1053	13	CL482318	CL482318 SAIL_359_
c	33	32.2	39.3	831	14	AG395160	AG395160 Mus muscu
c	34	32.2	39.3	872	11	AZ190012	AZ190012 SP_1016_A
	35	32.2	39.3	873	5	CK154648	CK154648 FGAS03335
c	36	32.2	39.3	974	10	DV057041	DV057041 MONTH14_0
	37	32.2	39.3	1038	2	BG177276	BG177276 602314466
	38	32	39.0	407	5	CI291021	CI291021 CI291021
c	39	32	39.0	690	2	BJ273105	BJ273105 BJ273105
	40	32	39.0	760	9	DR165226	DR165226 RTPHOS1_3
	41	32	39.0	786	4	CB658925	CB658925 OSJNEc15G
c	42	32	39.0	809	13	CW944356	CW944356 TcB26.2_H
	43	32	39.0	1038	8	CX106365	CX106365 BI126E07
	44	32	39.0	1064	12	CL135995	CL135995 ISB1-107F
	45	32	39.0	1101	14	CNS01523	AL104901 Drosophil

## EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	2923	TERT SAME promoter	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/09/18 09:36
L2	462	telomerase SAME promoter	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/09/18 09:37
L3	180	"human telomerase" SAME promoter	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/09/18 09:37
L4	183	hTERT SAME promoter	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/09/18 09:37
L5	87	"hTERT promoter"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/09/18 09:37
L6	8590	514/44.ccls.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/09/18 09:37
L7	62	I2 and I6	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/09/18 09:38
L8	20	I3 and I6	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/09/18 09:38
L9	21	I4 and I6	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/09/18 09:38
L10	13	I5 and I6	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/09/18 09:39
L11	3553	536/24.1.ccls.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/09/18 09:38



## EAST Search History

L12	15	I2 and I11	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/09/18 09:38
L13	8	I3 and I11	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/09/18 09:38
L14	6	I4 and I11	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/09/18 09:38
L15	3	I5 and I11	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/09/18 09:39
L16	0	I10 and I15	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/09/18 09:39
S1	2	("6777203").PN.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/09/18 07:59
S2	3	("6610839").PN.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/09/18 08:00
S3	2	("6777203").PN.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/09/18 09:36